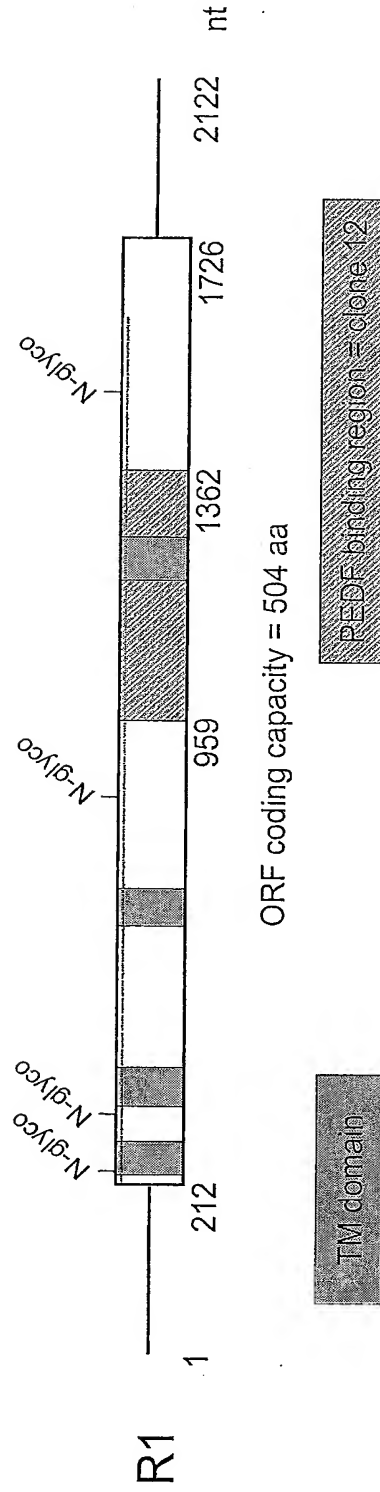


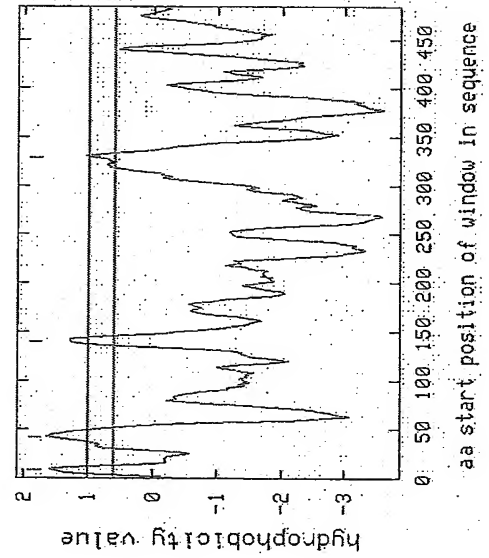
1/30

Figure 1.

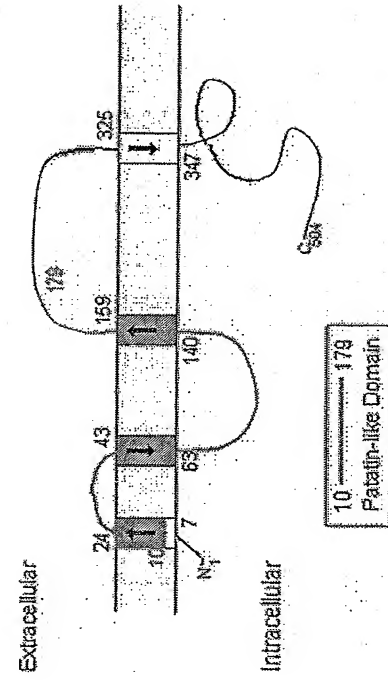
A.



B.



C.



2/30

Figure 1.

D.

R1
 adiponutrin

MFPRKTNWISFAGGFLGVYVGVASCLREHAPFLVANATHIYASAGALTATALTGTGCLGAGAKFIEVSKERKRFIG
 YDA RQ SL F H ATR H IRD RMLF HCVGLS I P EQTLQVLSDLVRK S NI

PLHPSFNLVKIIRSFLKVLPADESHASGRIGISLIRVSDGENVLISHFNSKDELIAQNVCSGFIPYCGLIPLPSLQGVRYV
 IF S FL QG C C NV QLI KI LV DFR VVD L C F S FR

DGGISDNLPYELKNTITVSPFSGESDIPQDSSTNIHELVRTNTSIQFNLRNLYRLSKA LFPPEPLVIREMCKQGYRDLR
 V V FIDA T P Y Y KVK FLHVDI KL LRUCTG L R FV DLK G I LR L AF

FLQRNGLLRPNP-LLALPP-----ARPHGPEDKQAVESQAE--DYSQLP--GEDH-ILEHLPARLNREALLE
 EEK IC Q G KSSSEGMDPEVAMPSWANMSLDSS SAAL RLEGD LL HLR SILPW ES DT SP AT S

ACVEPTDLLTTLNMLPVRLATAMMVPTLPLESALSFTIRLLEWLPDVPEDIRMMKEQT GSICQ YLVMRAKRLGRHLPS
 EMKD KGYMSKIC L I IMSYV L C V IAIVQ VT M D VL LQWV SQVTRVL CLLPASRSQM V

RLPEQVELRRVQSLPS-VPLSCAAYREALPGWNRNLSIGDALAKWHECORQLIIGLFCNTNVAFFPEALMRAPADPAPAPAD
 SSQOASPCTPE DW CWT C PKGCPAETKAAATPRSI RSS NFFIGNKVPAGAEGLS --- SFS EKSL-----

PASPQHLAGPAPILLSTPAPEARPVIGALGL SEQ ID NO:3
 ----- SEQ ID NO:27

E.

253 GLLNRPN PLLALPPARP HGEPRDKQAV ESAQAEYSQ LPGE 293 (SEQ ID NO:28)

450 T NVAFFPEALR MRAPADPAPA PADPASPOHQ LAGPAPILLST PAPEARPVIG ALGL 504 (SEQ ID NO:29)

Figure 1.

F.

Homologous patatin phospholipase A (PLA) active site in R1: **S47** and **D166**

Active site serine

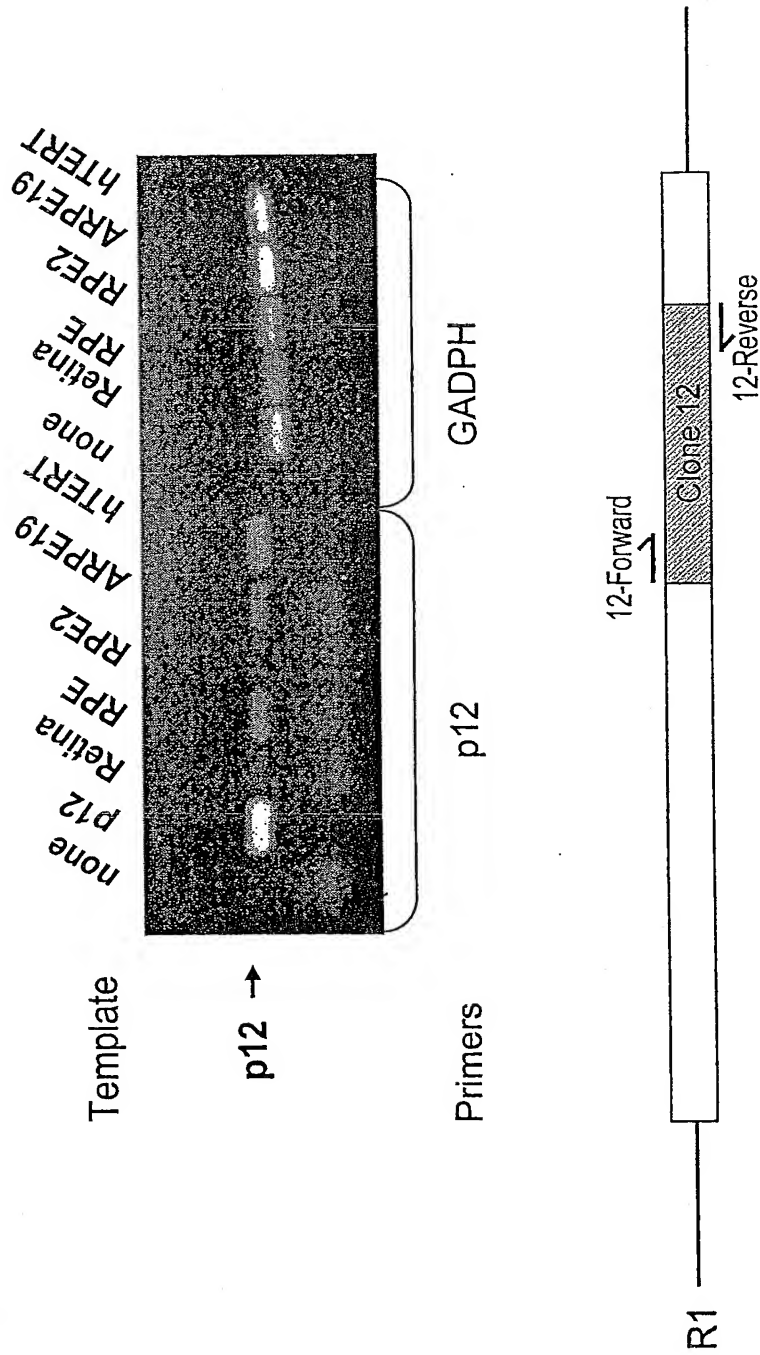
NA THYGA	SAGA	LTA	R1	SEQ ID NO: 30
YF DVI	GGT	STGG	LLT Patatin B2	SEQ ID NO: 31
CA TYV	AGL	SGST	WYM cPLA2	SEQ ID NO: 32

Active site aspartic

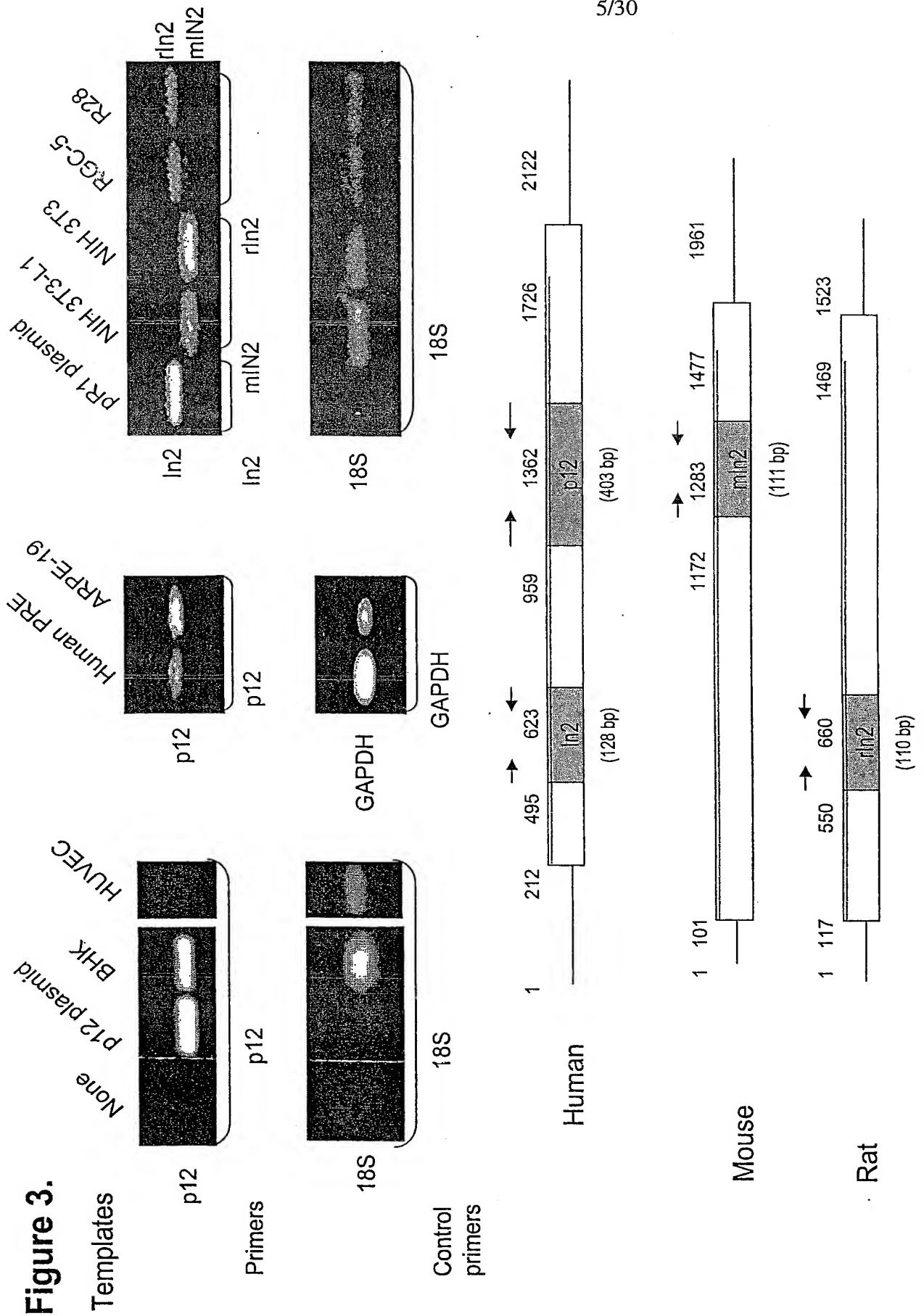
SLQ GVR	YVD	GGIS	DNLPLYE	R1	SEQ ID NO: 33
ARY EFN	LVD	GAVA	TVGDPAL	Patatin B2	SEQ ID NO: 34
KSK KIH	VVD	SGL-	TFNLPYP	cPLA2	SEQ ID NO: 35

4/30

Figure 2.

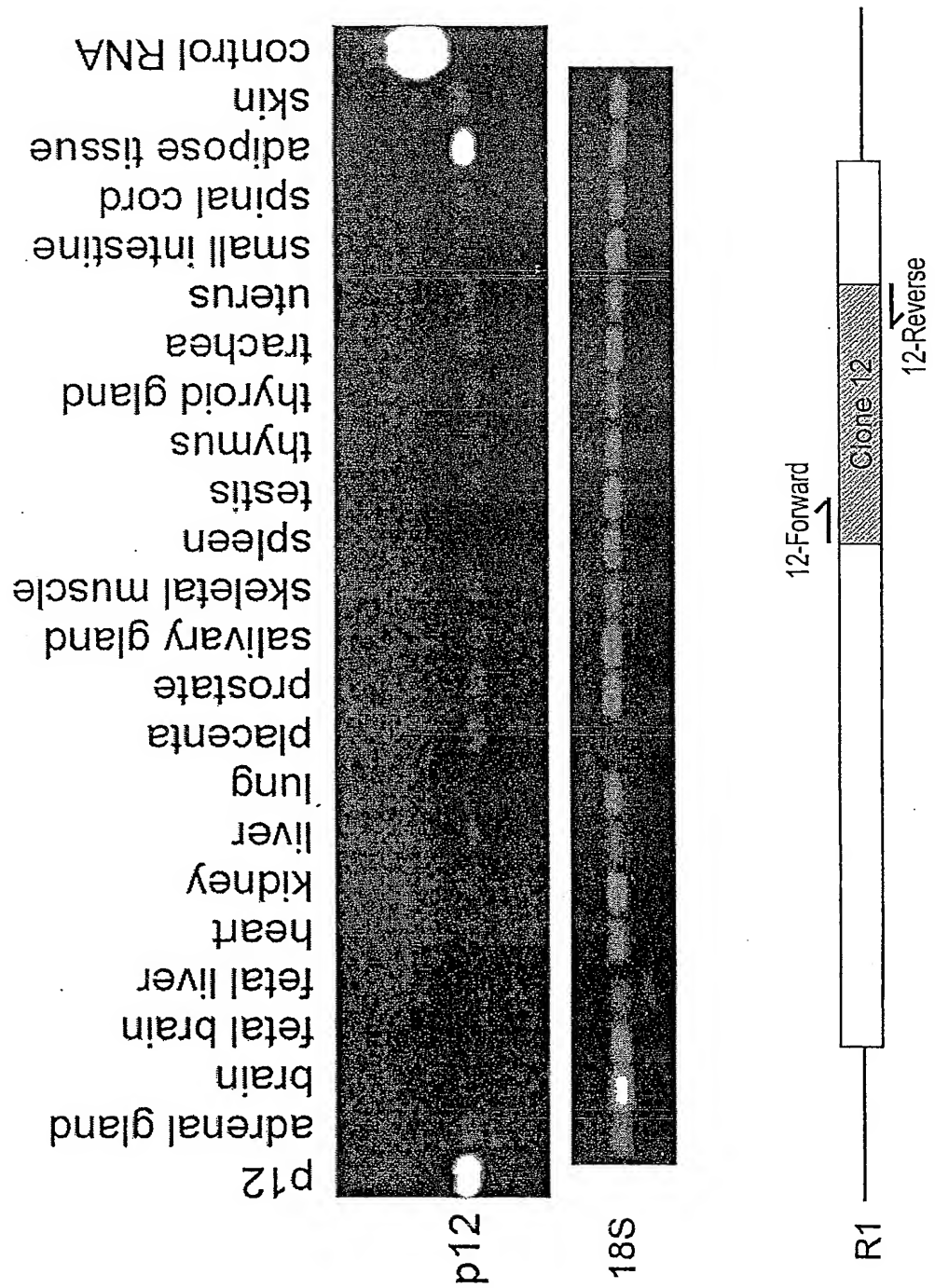


5/30



6/30

Figure 4.



7/30

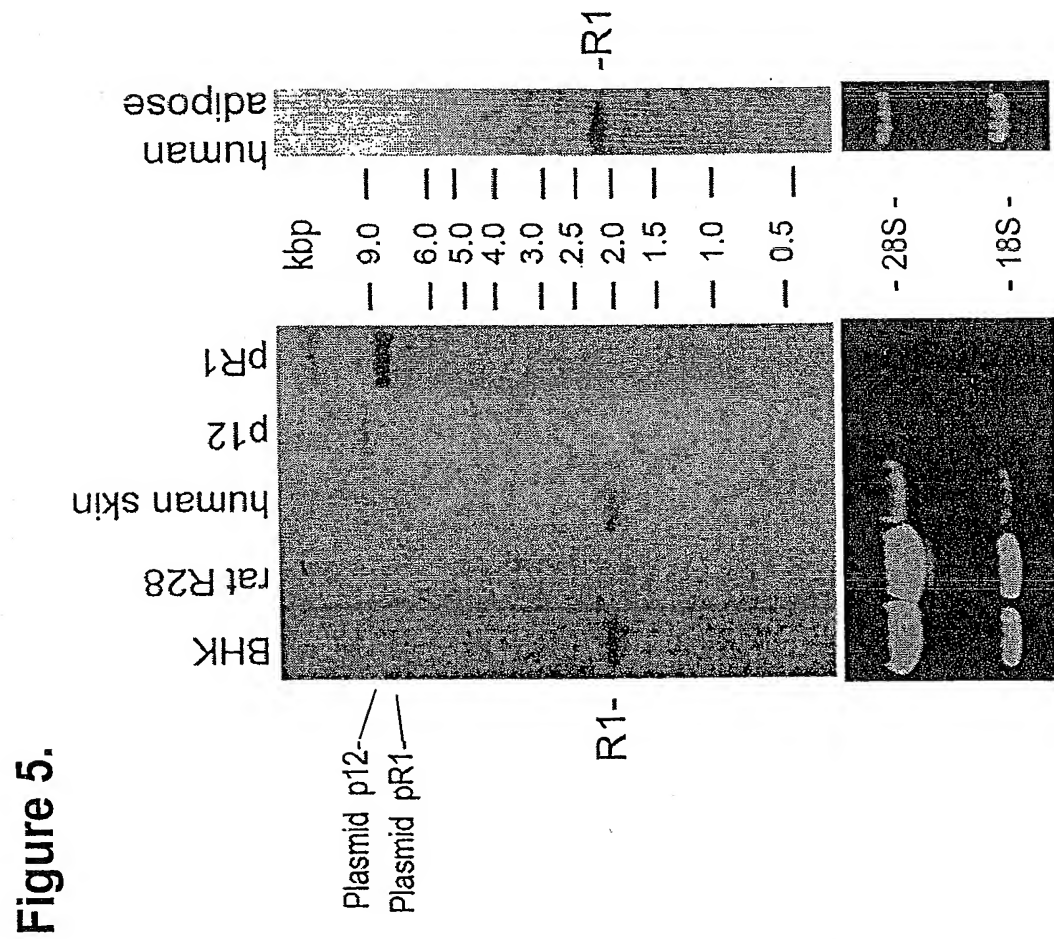
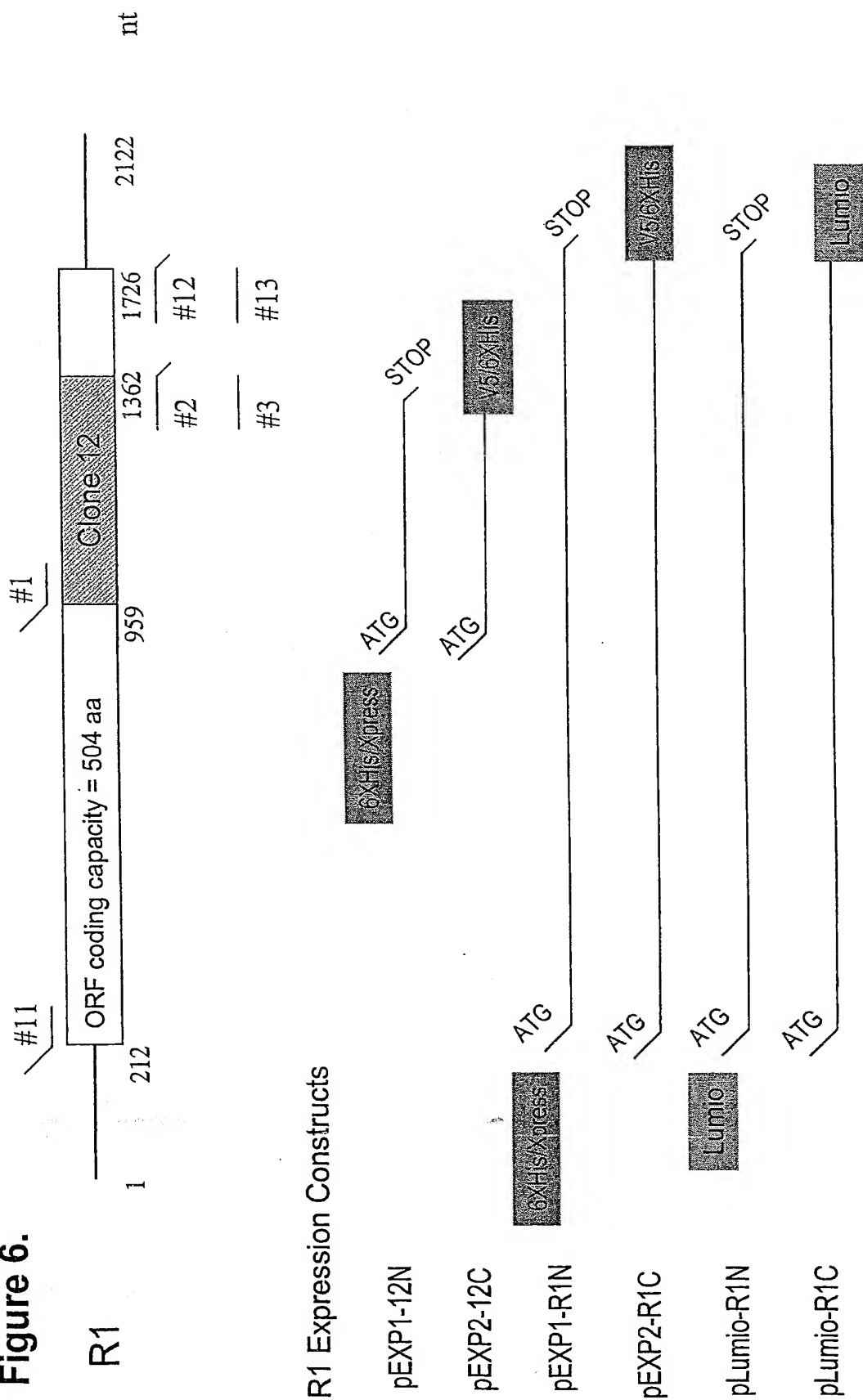
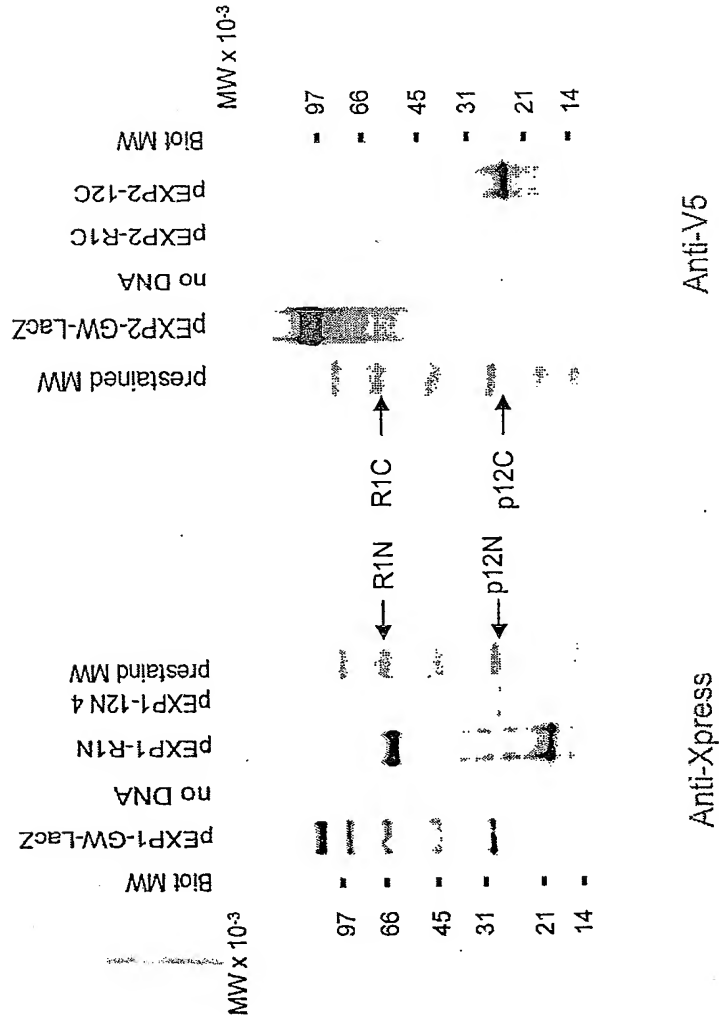


Figure 6.



9/30

Figure 7.

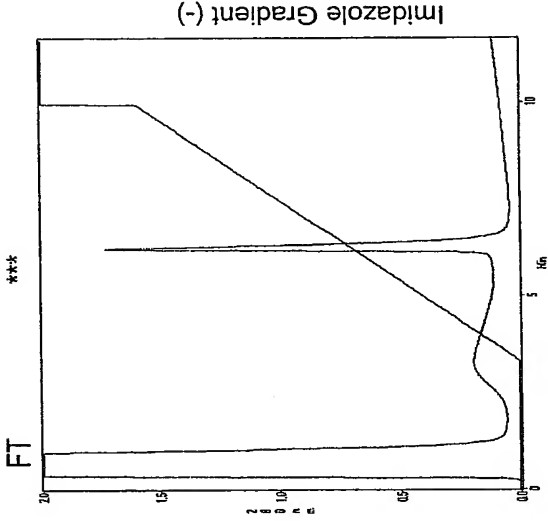


10/30

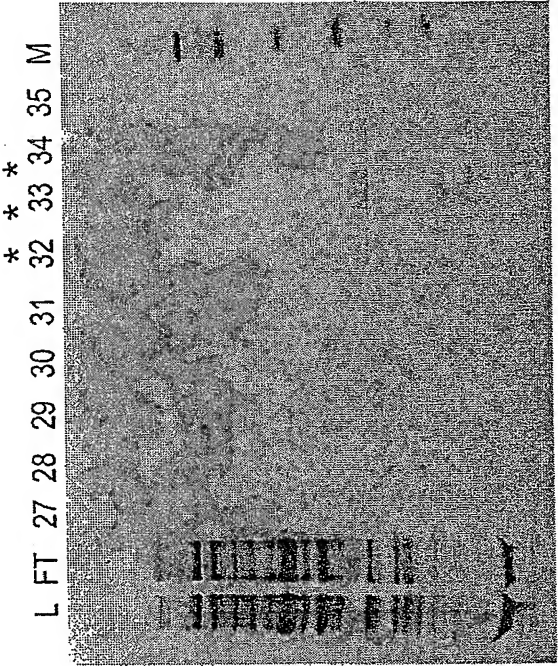
Figure 8.

A. p12

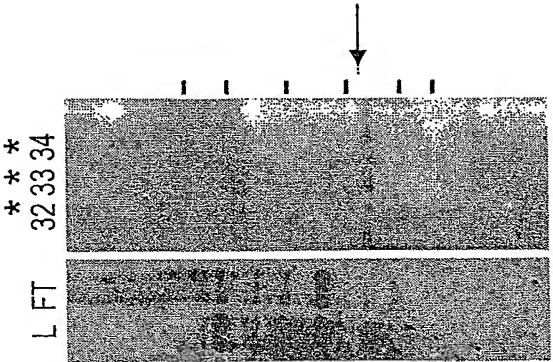
Chromatogram



SDS-PAGE
(Magic Blue stained gel)



Western (Ab-His)

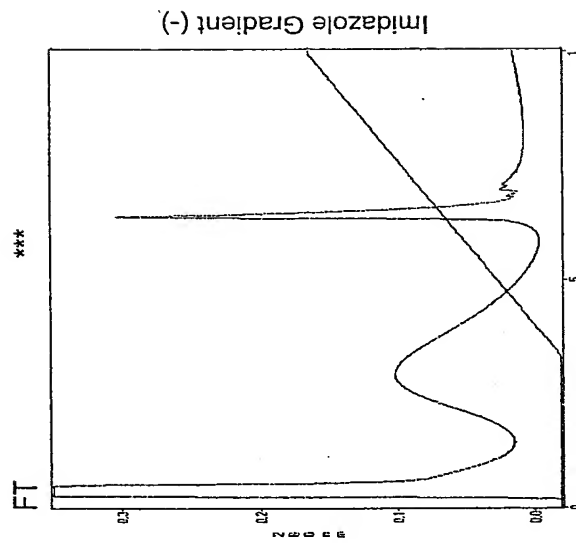


11/30

Figure 8.

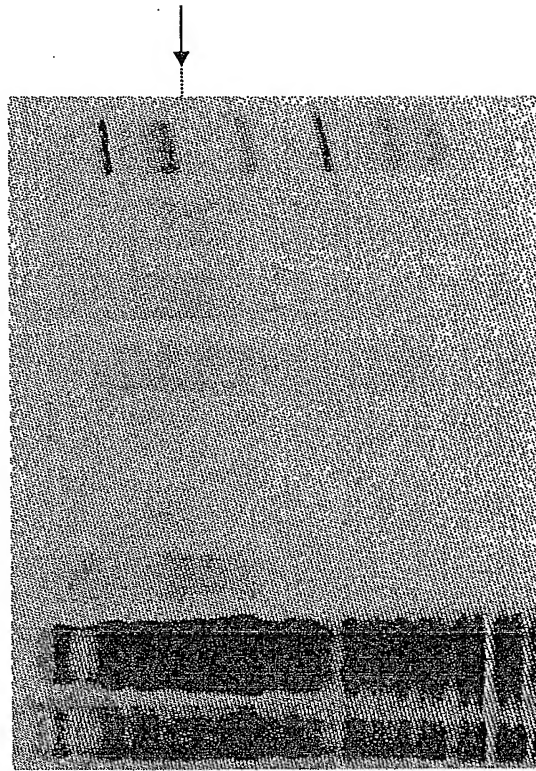
B. R1

Chromatogram



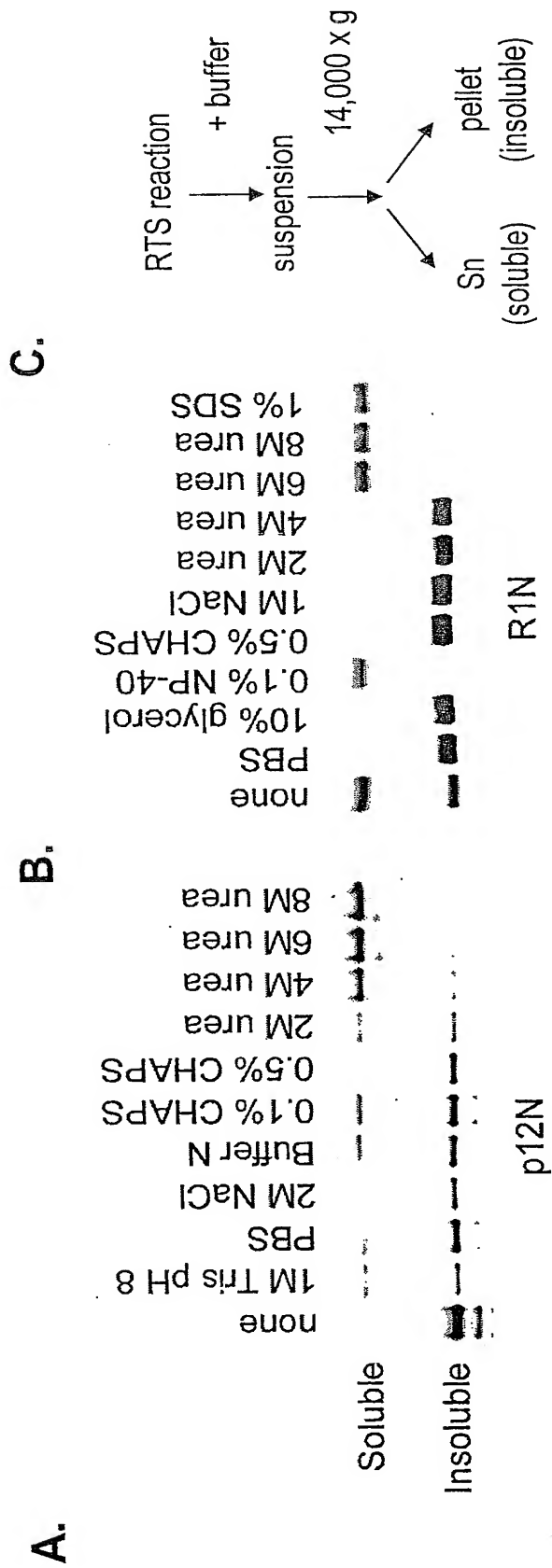
SDS-PAGE (Coomassie Blue stained gel)

L FT 13 14 15 16 17 18 M



12/30

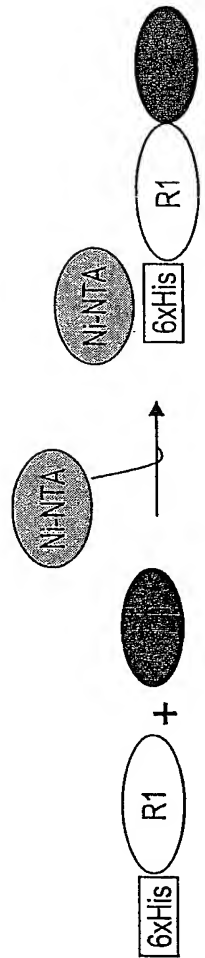
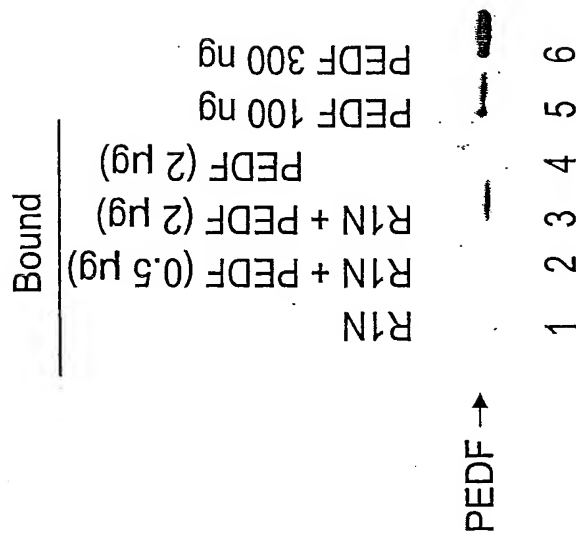
Figure 9.



13/30

Figure 10.

A. His-tag pull-down



B. complex formation

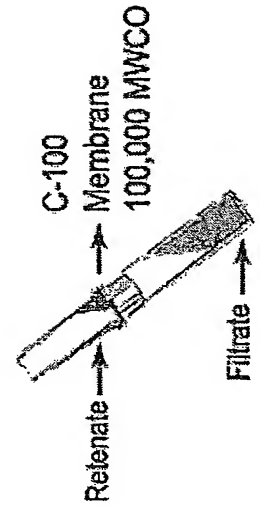
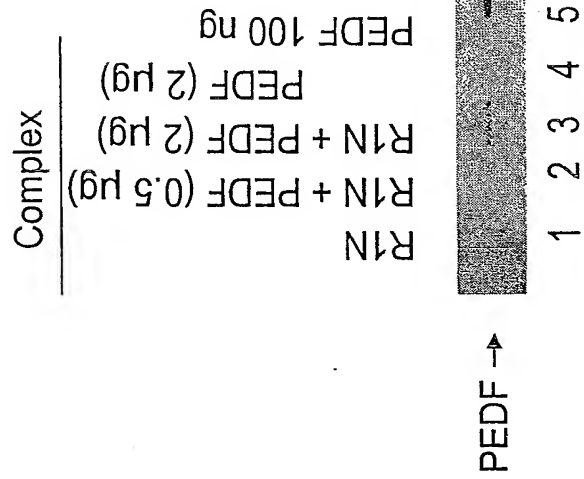
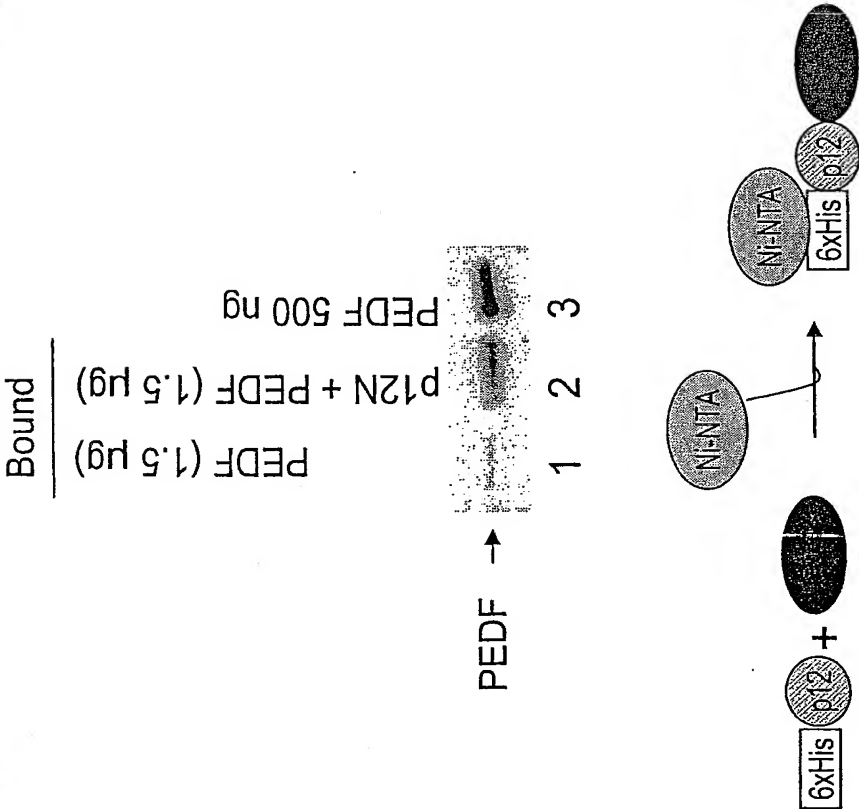


Figure 11.

A.



B.

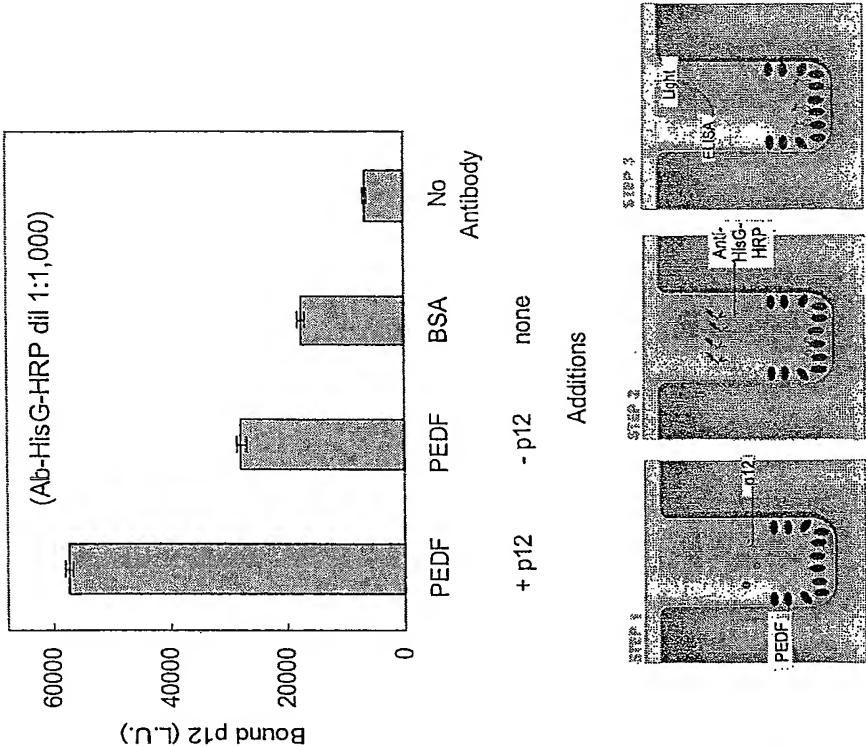


Figure 12.

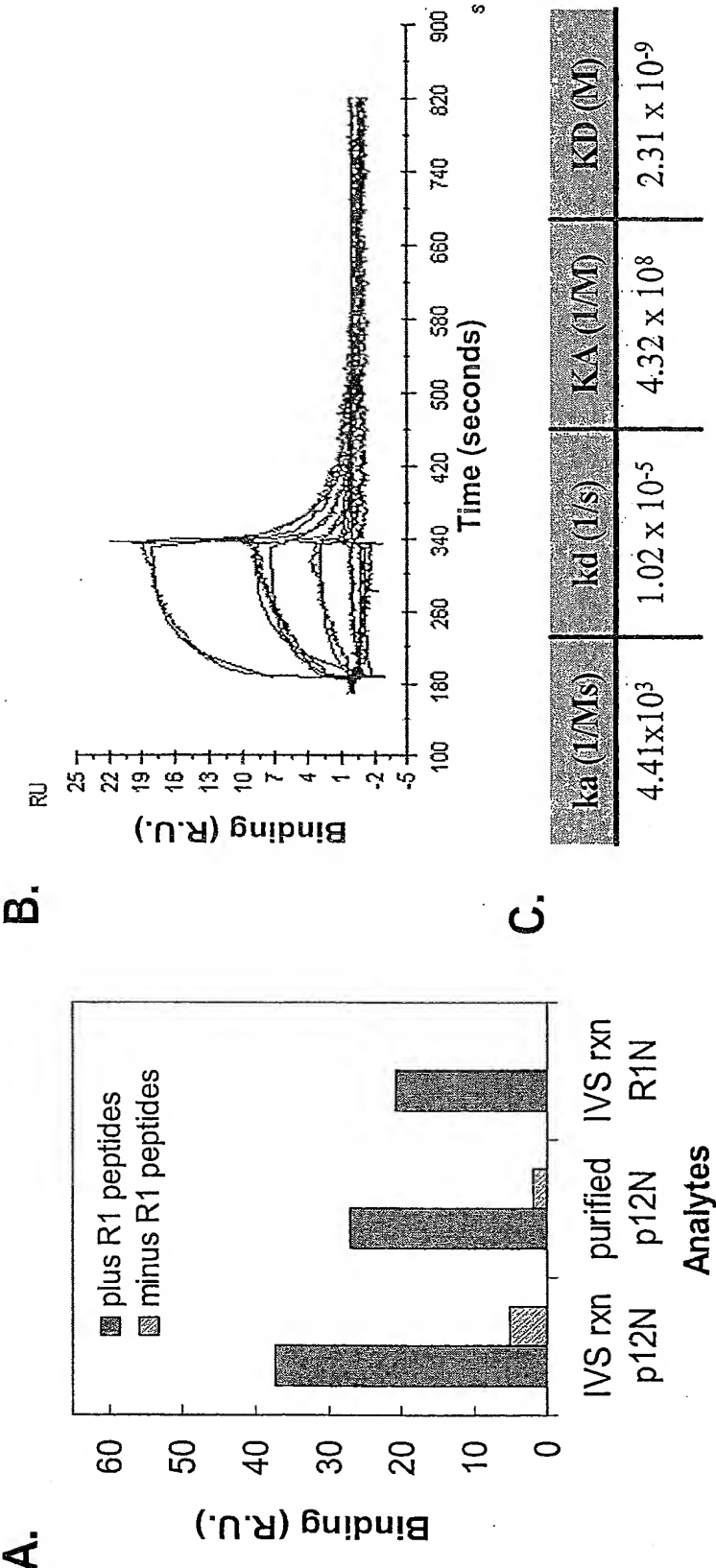
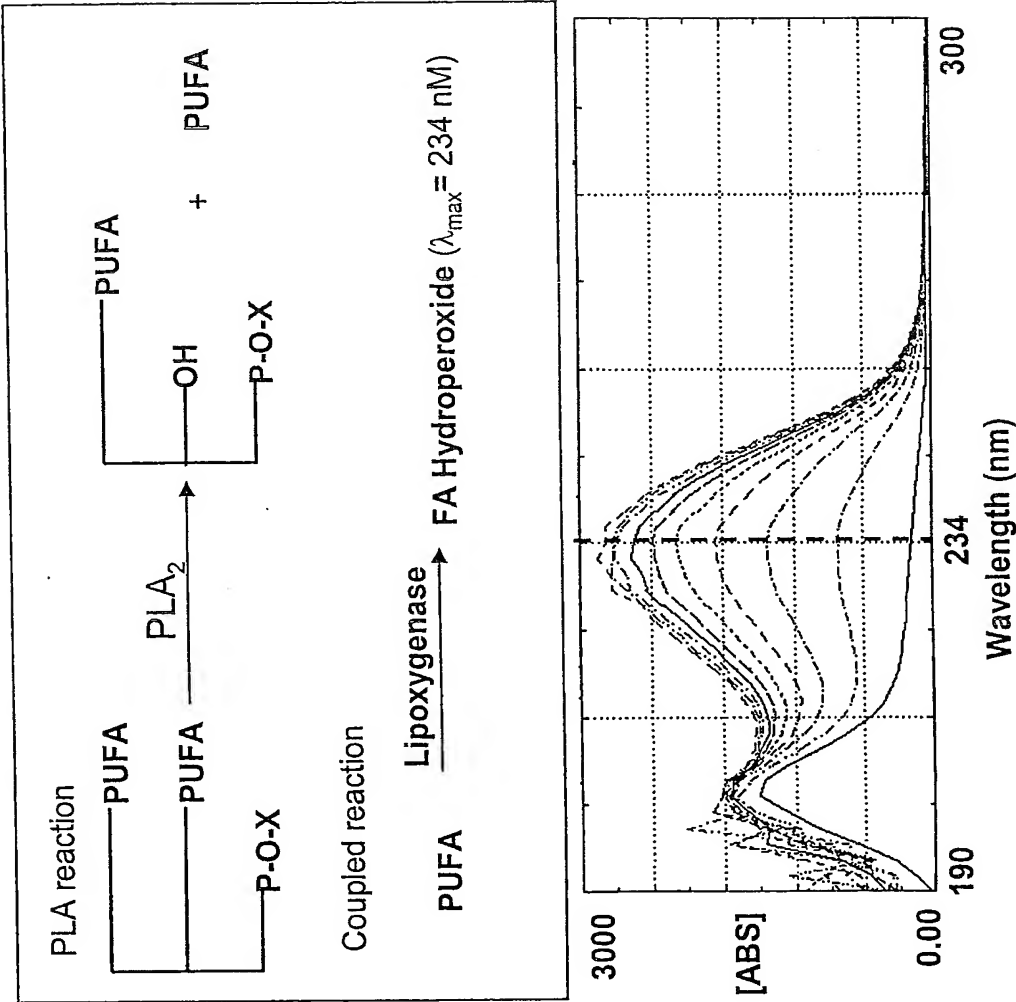


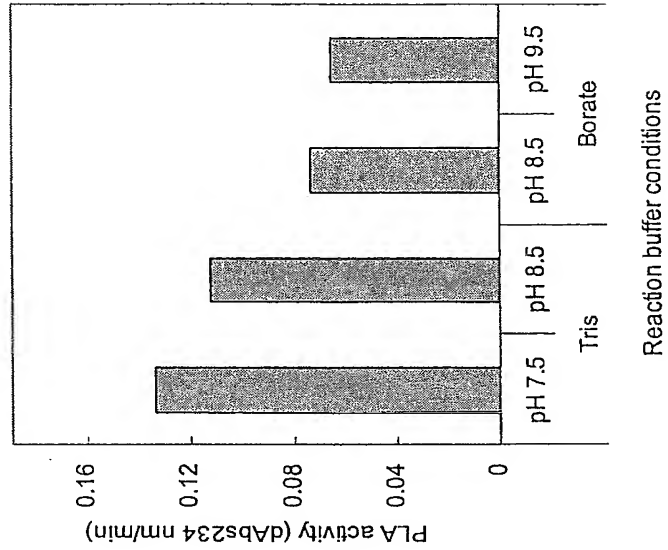
Figure 13.
A.



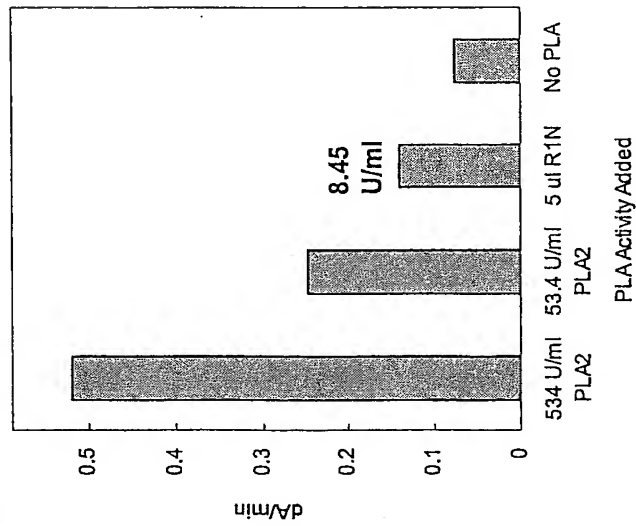
17/30

Figure 13.

C.

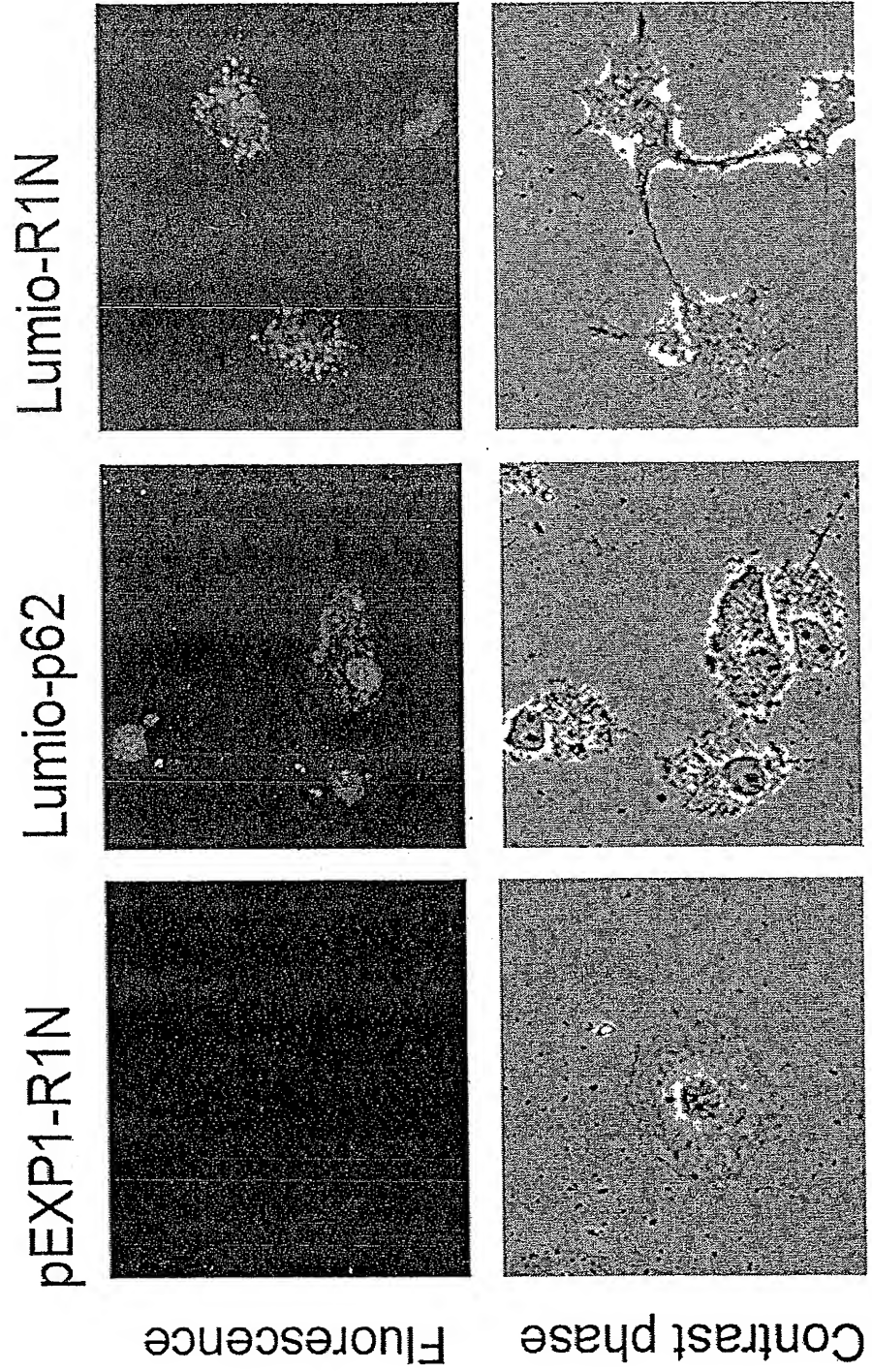


B.



18/30

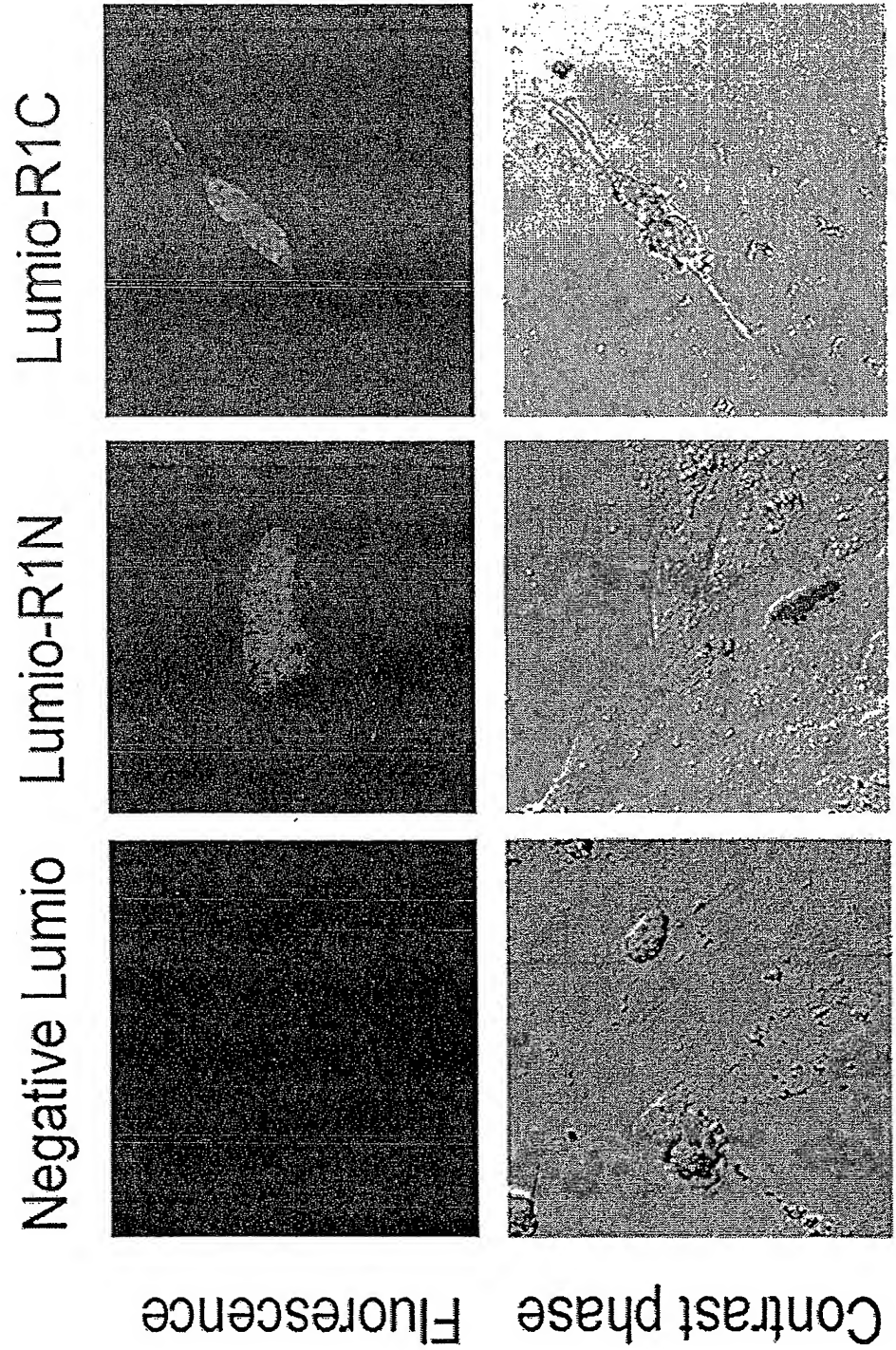
Figure 14.
A. COS-7 cells



19/30

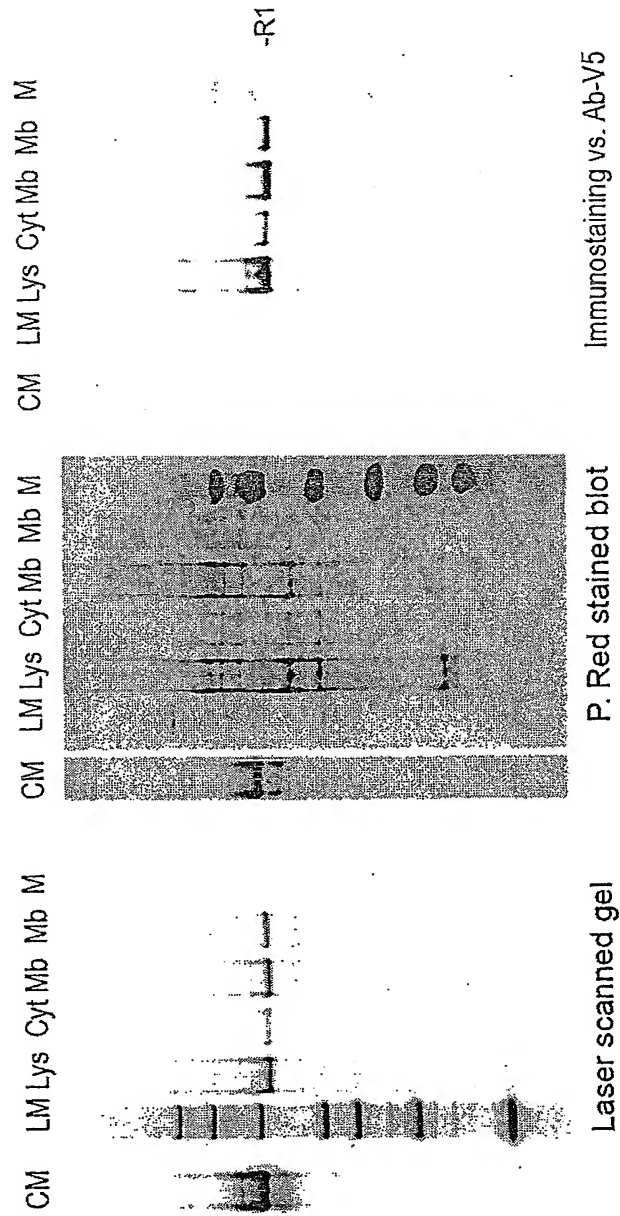
Figure 14.

B. Retinal ganglion RGC-5 cells



20/30

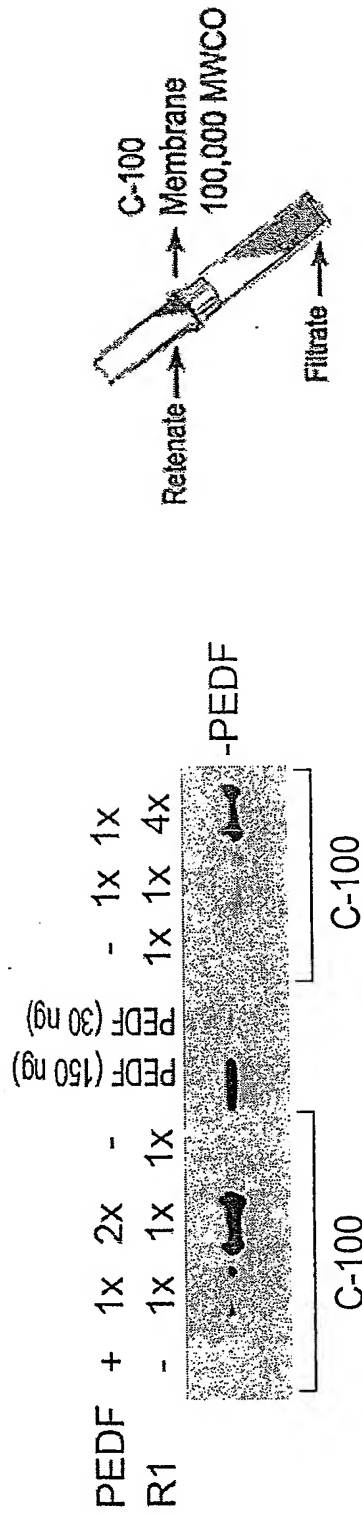
Figure 15.



LM= Lumio markers, M = MW standards CM, conditioned media; Lys, Lysate; Cyt, cytosolic; Mb, membrane fractions

21/30

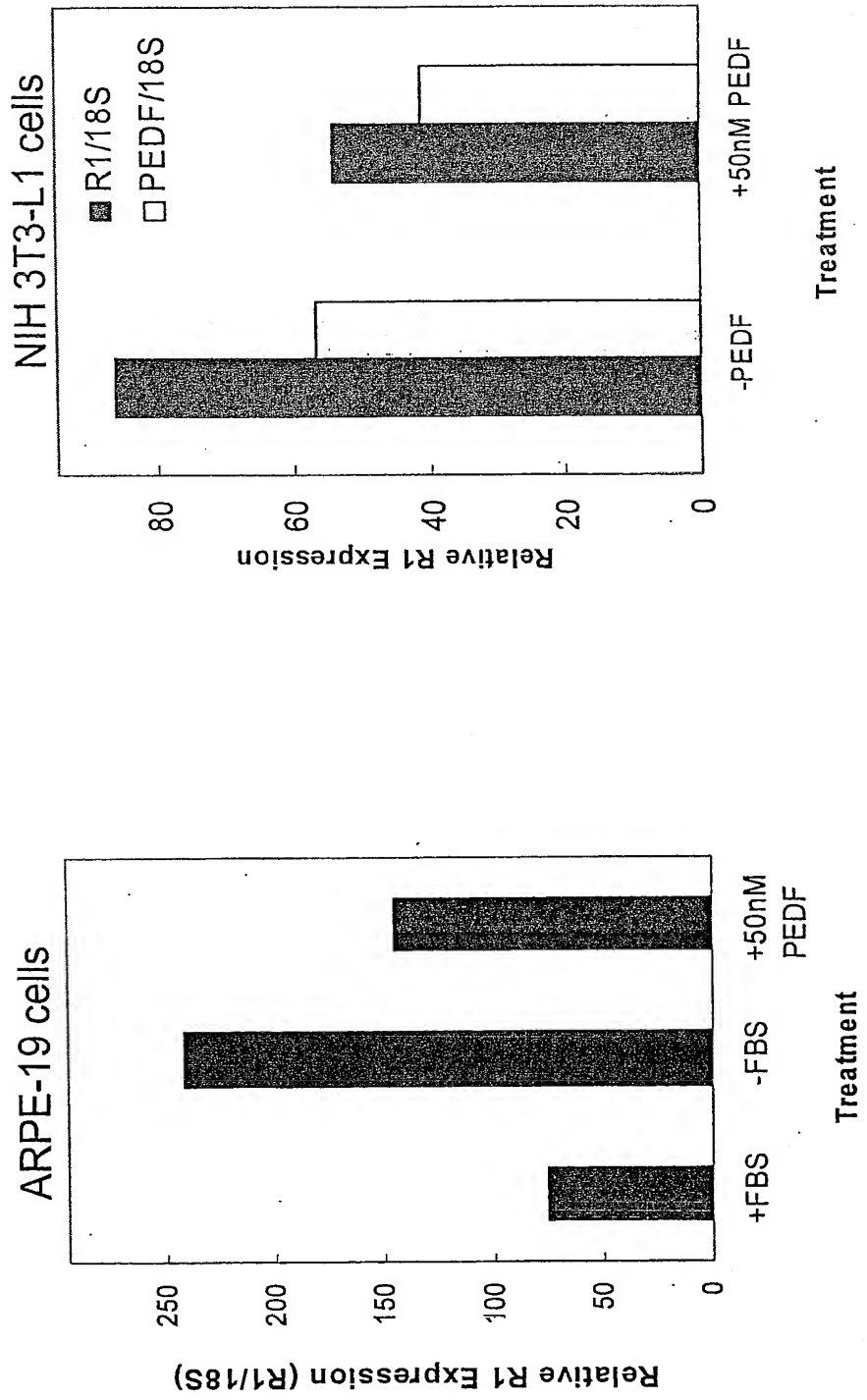
Figure 16.



22/30

Figure 17.

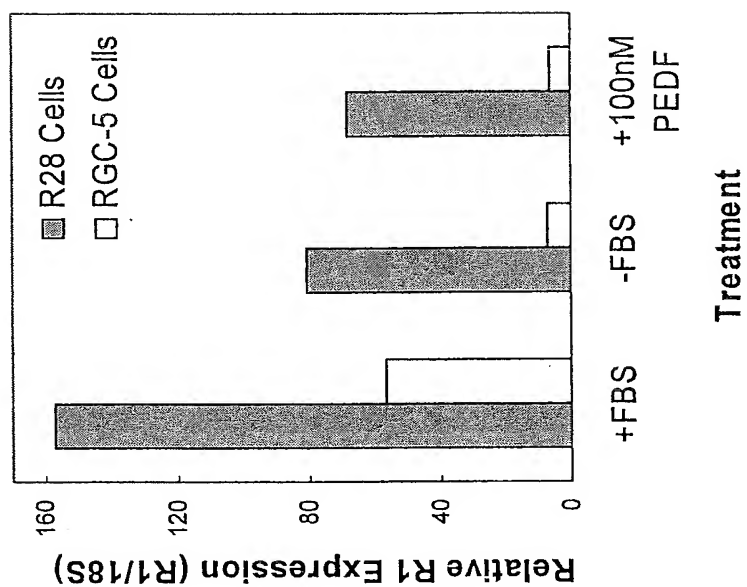
A.



23/30

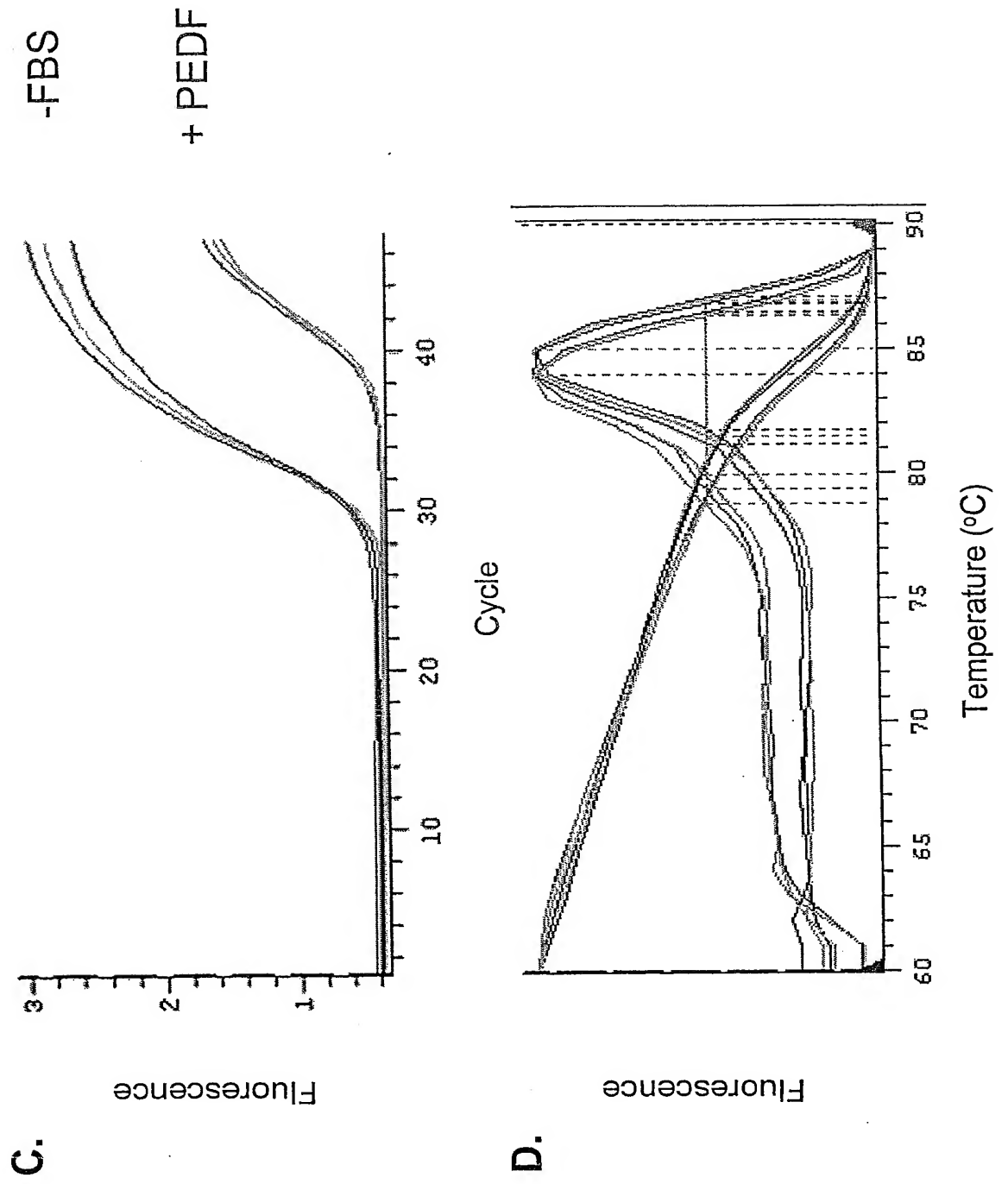
Figure 17.

B.



24/30

Figure 17.



25/30

Figure 18.

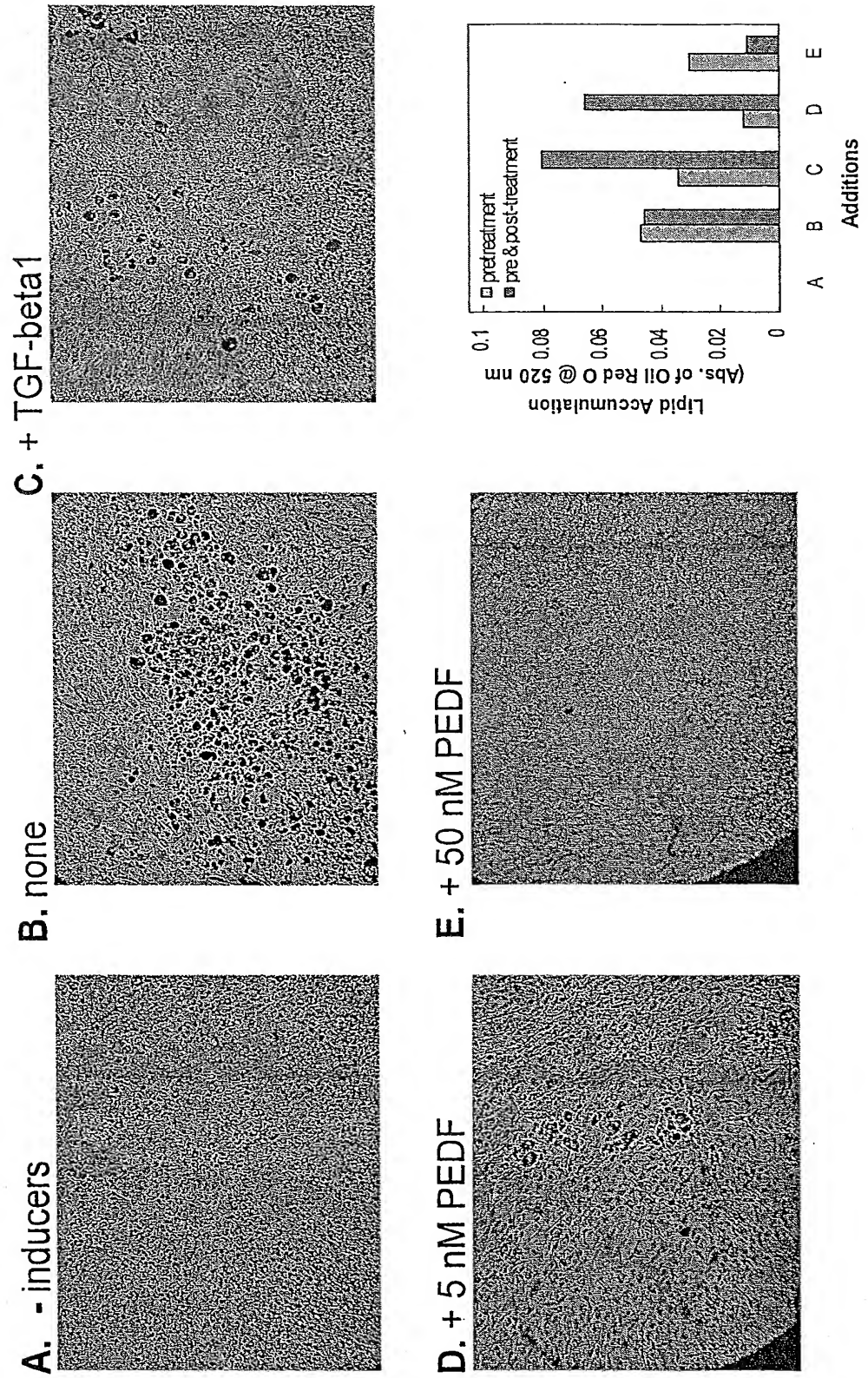


Figure 19.

gi 26327465 dbj BAC27476.1	MFPRETKNWISFAGCGFLGVYHIGVASCLREHAPFLVANATHIYGASAGA	50
gi 34861242 ref XP_341961.1	MFPRETKNWISFAGCGFLGVYHIGVASCLREHAPFLVANATHIYGASAGA	50
gi 16878147 gb AAH17280.1	MFPRETKNWISFAGCGFLGVYVGVASCLREHAPFLVANATHIYGASAGA *****.*****.:*****.*****.	50
gi 26327465 dbj BAC27476.1	LTATALVTGACLGEAGANIEVSKEARKRFLGPLHPSFNLVKTIIRGCLLK	100
gi 34861242 ref XP_341961.1	LTATALVTGACLGEAGANIEVSKEARKRFLGPLHPSFNLVKTIIRGCLLK	100
gi 16878147 gb AAH17280.1	LTATALVTGVCLEAGEAKFIEVSKEARKRFLGPLHPSFNLVKIIRSFLK *****.*****.:*****.***,	100
gi 26327465 dbj BAC27476.1	TLPADCHERANGRLGISLTRVSDGENVIISHFSKDELIQANVCSTFIPV	150
gi 34861242 ref XP_341961.1	TLPADCHTRASGRLGISLTRVSDGENVIISHFSKDELIQANVCSTFIPV	150
gi 16878147 gb AAH17280.1	VLPADSHEHASGRLGISLTRVSDGENVIISHFNSKDELIQANVCSGFIPV .****,* :*,*****.*****.***	150
gi 26327465 dbj BAC27476.1	YCGLIPPTLQGVRYVDGGISDNPLPYELKNTITVSPFSGESDIPCQDSST	200
gi 34861242 ref XP_341961.1	YCGLIPPTLQGVRYVDGGISDNPLPYELKNTITVSPFSGESDIPCQDSST	200
gi 16878147 gb AAH17280.1	YCGLIPPSLQGVRYVDGGISDNPLPYELKNTITVSPFSGESDIPCQDSST *****.:*****.*****	200
gi 26327465 dbj BAC27476.1	NIHELRTNTSIQFNLRNLYRLSKALFPPEPMVLREMCKQGYPDGLRFLR	250
gi 34861242 ref XP_341961.1	NIHELRTNTSIQFNLRNLYRLSKALFPPEPMVLREMCKQGYPDGLRFLR	250
gi 16878147 gb AAH17280.1	NIHELRTNTSIQFNLRNLYRLSKALFPPEPLVLREMCKQGYPDGLRFLQ *****.:*****.:*****:	250
gi 26327465 dbj BAC27476.1	RNGLLNQPNPLALPPVPVQEEDAEAAVEERAGEEDQLQPYRKDRILE	300
gi 34861242 ref XP_341961.1	RNGLLNQPNPLALPPVPVQEEDAEAAVTEERTGGED-----RILE	292
gi 16878147 gb AAH17280.1	RNGLLNRPNPLALPPARPHPGDKDQSAESAQEDYSQLP--GEDHILE *****.:*****.* : : : * . : : : *	298
gi 26327465 dbj BAC27476.1	HLPARLNEALLEACVEPKDMLTTLSNMPLPVRLATAMMVFYTLPLESAVSF	350
gi 34861242 ref XP_341961.1	HLPARLNEALLEACVEPKDMLTTLSNMPLPVRLATAMMVFYTLPLESAVSF	342
gi 16878147 gb AAH17280.1	HLPARLNEALLEACVEPTDLLTTSNMPLPVRLATAMMVFYTLPLESALSF *****.***.:*****.***	348
gi 26327465 dbj BAC27476.1	TIRLLEWLDPVEDIRWMKEQTGSICQYLVMRAKRKLGDHLPSRLSEQVE	400
gi 34861242 ref XP_341961.1	TIRLLEWLDPVEDIRWMKEQTGSICQYLVMRAKRKLGDHLPSRLSEQVE	392
gi 16878147 gb AAH17280.1	TIRLLEWLDPVEDIRWMKEQTGSICQYLVMRAKRKLGRHLPSRLPEQVE *****.:*****.*****.***	398
gi 26327465 dbj BAC27476.1	LRRAQSLPSVPLSCATYSEALPNWVRNNLSLGDALAKWEECQRQLLGLF	450
gi 34861242 ref XP_341961.1	LRRAQSLPSVPLSCATYSEALPNWVRNNLSLGDALAKWEECQRQLLGLF	442
gi 16878147 gb AAH17280.1	LRRVQSLSVPLSCAAYREALPGWMRNNSLGDALAKWEECQRQLLGLF ***.*****:* *****:*****.*****	448
gi 26327465 dbj BAC27476.1	CTNVAFPPDALRMRAPAS--PTAADPATPDQPGLPPC-----	486
gi 34861242 ref XP_341961.1	CTNVAFPPDALRMRAPAS--PTATDPATPDQPSGLPPC-----	478
gi 16878147 gb AAH17280.1	CTNVAFPEALRMRAPADPAPAPADPASPOHQLAGPAPLLSTPAPEARPV *****.:*****.* : : : * . . *	498
gi 26327465 dbj BAC27476.1	----- (SEQ ID NO:14)	
gi 34861242 ref XP_341961.1	----- (SEQ ID NO:17)	
gi 16878147 gb AAH17280.1	IGALGL 504 (SEQ ID NO:3)	

27/30

Figure 20. (1 of 4)

CLUSTAL W (1.82) multiple sequence alignment

```
gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01. GGCACGAGGGCGGCCAGTCAGACGCGAGGCAGCCCCAAAGCCTGAACAG 50

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 GCAGGGCCAGACCCAGCTTCTTCGCCTCCGCCAGCGGGGACCCCGAGCTA 100

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 GAGCCGCGAGCGGGACCTGCCCGGCCCGCGCTCCAGCGAGCGAGCGGCGA 150

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 -----TCCTCTGCCTCCCGGCACAGCGTCTCCGCCTCCG 34
GAGCCGCGAGCGGGACCTGCCCGGCCCGCGCTCCAGCGAGCGAGCGGCGA 150

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 -----GGAGACCCCAAGGTATCGA-GACTGCGGGACCCACTGCCCGCAGG 44
CCGGCGGGGACCCAGGTTATCAA-GACTGCGGGACCCACTGCCCGCAGG 83
GCAGGCGGCTCACAGAGGCCCTGGCCGCCACGGAACCCGGGGCCCGCGCG 200
* * * * *

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 ACATCGAGTCACGATGTTCCCGAGGGAGACCAAGTGGAACATCTCATTCG 94
ACGTCTAATACGATGTTCCCAAGGGAGACCAAGTGGAACATCTCGTTTCG 133
CCGCC--GCCGCGATGTTTCCCGCGAGAAAGCGTGAACATCTCGTTTCG 248
* * * * *

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 CTGGCTGCGGCTTCTCTCGGGGTCTACCACTTGCGCTGGCCTCTCGCCTC 144
CTGGCTGCGGCTTCTCTCGGGGTCTACCACTTGAGTGGCCTCTCGCCTC 183
CGGCTGCGGCTTCTCTCGGCGTCTACTACGTGCGCTGGCCTCTCGCCTC 298
* * * * *

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 CGTGAGCAGCGGCCCTTCTGTTGGCCAAACGCCACTCACATCTACGGAGC 194
CGTGAGCAGCGGCCCTTCTGTTGGCCAAACGCCACTCACATCTACGGAGC 233
CGCAGCAGCGGCCCTTCTGTTGGCCAAACGCCACTCACATCTACGGAGC 348
** * * * *

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 CTCGGCAGGGGCGCTACCGCCACAGCGCTGGTCACTGGGGCCTGCCTGG 244
CTCGGCAGGGGCGCTTACCGCCACAGCGCTGGTCACTGGGGCCTGCCTGG 283
CTCGGCCGGGCGCTCACGGCCACGGCGCTGGTCACTGGGGCTGCCTGG 398
*****

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 GTGAAGCAGGTGCCAACATTATTGAGGTGTCCAAGGAGGCCCGGAAGCGG 294
GCGAAGCGGGTGCCAACATTATTGAGGTGTCCAAGGAGGCTCGGAAGCGG 333
GTGAGGCTGGTGCCAAAGTTCAATTGAGGTATCTAAAGAGGCCCGGAAGCGG 448
* * * * *

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 TTCTTGGGTCTCTGCATCCCTCCTTCAACCTGGTGAAGACCATCCGTGG 344
TTCTTGGGTCTCTGCATCCCTCCTTCAACCTGGTGAAGACCATCCGTGG 383
TTCTTGGGTCTCTGCATCCCTCCTTCAACCTGGTGAAGATCATCCGCAG 498
*****

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 CTGTCTACTAAGACCCCTGCCTGCTGATTGCCATGAGCGCGCCAAATGGAC 394
TTGTCTACTGAAGACCCCTGCCTGCTGATTGCCACACGCGTGCCAGCGGAC 433
TTTCTGCTGAAGGCTCTGCCTGCTGATAGCCATGAGCATGCCAGTGGGC 548
* * * * *

gi|26327464|dbj|AK031609.1|-----
gi|34861241|ref|XM_341960.1|-----
gi|16878146|gb|BC017280.1|BC01 GCCTGGGCATCTCCCTGACTCGTGTTCAGACGGAGAGAACGTCATCATA 444
GCCTGGGCATCTCCCTGACTCGAGTTTCGGATGGAGAGAAATGTCATCATA 483
GCCTGGGCATCTCCCTGACCCGCGTGTACAGACGGCGAGAAATGTCATCATA 598
*****
```

28/30

Figure 20. (2 of 4)

gi 26327464 dbj AK031609.1	TCCCACTTTAGCTCCAAGGATGAGCTCATCCAGGCCAATGTCTGCAGCAC	494
gi 34861241 ref XM_341960.1	TCCCACTTTAGCTCCAAGGATGAGCTTATCCAGGCCAATGTTTGCAGCAC	533
gi 16878146 gb BC017280.1 BC01	TCCCACTTCAACTCCAAGGACGAGCTCATCCAGGCCAATGTCTGCAGCGG	648
	*** **	
gi 26327464 dbj AK031609.1	ATTATCCCGGTGTACTGTGGCCTCATTCCTACCTCCAAGGGGTGC	544
gi 34861241 ref XM_341960.1	TTTATCCCTGTGTACTGTGGCCTCATTCCTACCTTCAAGGGGTGC	583
gi 16878146 gb BC017280.1 BC01	TTTCATCCCGGTGTACTGTGGCCTCATTCCTCCCTCCAGGGGTGC	698
	** **	
gi 26327464 dbj AK031609.1	GCTATGTGGATGGCGGCATTTAGACAACTTGCCACTTTATGAGCTGAAG	594
gi 34861241 ref XM_341960.1	GCTATGTGGATGGCGGCATTTAGACAACTTGCCACTTTATGAGCTGAAG	633
gi 16878146 gb BC017280.1 BC01	GCTACGTGGATGGTGGCATTTCAGACAACTTGCCACTTATGAGCTTAAG	748

gi 26327464 dbj AK031609.1	AATACCATCACAGTGTCCCCATTCTCAGGCGAGAGTGACATCTGCCCTCA	644
gi 34861241 ref XM_341960.1	AATACCATCACAGTGTCCCCATTCTCAGGCGAGAGTGACATCTGCCCTCA	683
gi 16878146 gb BC017280.1 BC01	AACACCATCACAGTGTCCCCCTTCTCGGCGAGAGTGACATCTGTCGCA	798
	** **	
gi 26327464 dbj AK031609.1	GGACAGCTCCACCAACATCCACGAGCTTCGCGTCACCAACACCAGCATCC	694
gi 34861241 ref XM_341960.1	AGACAGCTCCACCAACATCCACGAACTTCGATATCACCACACCAGCATCC	733
gi 16878146 gb BC017280.1 BC01	GGACAGCTCCACCAACATCCACGAGCTCGCGGTCACCAACACCAGCATCC	848
	***** **	
gi 26327464 dbj AK031609.1	AGTTCAACCTTCGCAATCTCTACCGCCTCTCGAAGGCTCTCTTCCCGCCA	744
gi 34861241 ref XM_341960.1	AATTCAACCTTCGCAATCTCTACCGCCTCTCGAAGGCTCTCTTCCCGCCA	783
gi 16878146 gb BC017280.1 BC01	AGTTCAACCTTCGCAACCTCTACCGCCTCTCGAAGGCCCTCTTCCCGCGG	898
	* **	
gi 26327464 dbj AK031609.1	GAGCCCATGGTCTCTCCGAGAGATGTGCAACAGGGCTACAGAGATGGACT	794
gi 34861241 ref XM_341960.1	GAGCCCATGGTCTCTCCGAGAGATGTGCAACAGGGCTACAGAGATGGACT	833
gi 16878146 gb BC017280.1 BC01	GAGCCCCTGGTCTCGAGAGATGTGCAAGCAGGATACCGGGATGGCCT	948
	***** **	
gi 26327464 dbj AK031609.1	TCGATTCCTTAGGAGGAATGGCCTACTGAACCAACCAACCCCTTGCTGG	844
gi 34861241 ref XM_341960.1	TCGATTCCTTAGGAGGAATGGCCTACTGAACCAACCAACCCCTTGCTGG	883
gi 16878146 gb BC017280.1 BC01	GCGCTTCTGCGGGAACGGCCTCTGAACCGGCCCAACCCCTTGCTGG	998
	** **	
gi 26327464 dbj AK031609.1	CACTGCCCCAGTTGTCCCCAGGAAGAGGATGCAGAGGAAGCTGTGTG	894
gi 34861241 ref XM_341960.1	CACTGCCCCCGTTGTCCCCAGGAAGAGGATGCAGAGGAAGCTGCCGTG	933
gi 16878146 gb BC017280.1 BC01	CGTTGCCCCCGCCCCGCCCCACGG-----CCCAGAGGACAAGGACCAG	1042
	* **	
gi 26327464 dbj AK031609.1	GTGGAGGAGAGGGCTGGAGAGGAGGATCAATTGCAGCCTTATAGAAAAGA	944
gi 34861241 ref XM_341960.1	ACTGAGGAGAGGACTGGAGGGGAGGATC-----	961
gi 16878146 gb BC017280.1 BC01	GCAGTGGAGAGCGCCCAAGCGGAGGATTACTGCGAGCTGCCGGGAGAAGA	1092
	* **	
gi 26327464 dbj AK031609.1	TCGAATTCTAGAGCACCTGCCTGCCAGACTCAATGAGGCCCTGCTGGAGG	994
gi 34861241 ref XM_341960.1	--GGATTCTAGAGCACCTGCCTGCCAGACTCAACGAGGCCCTGCTGGAGG	1009
gi 16878146 gb BC017280.1 BC01	TCACATCCTGAGAGCACCTGCCCGCCCGGCTCAATGAGGCCCTGCTGGAGG	1142
	** **	
gi 26327464 dbj AK031609.1	CCTGTGTGGAACCAAGGACCTGATGACCACCCCTTCCAACATGCTACCA	1044
gi 34861241 ref XM_341960.1	CCTGTGTGGAACCGAAGACCTGATGACCACCCCTTCCAACATGCTGCCA	1059
gi 16878146 gb BC017280.1 BC01	CCTGCGTGGAGCCCACGGACCTGCTGACCACCCCTCTCCAACATGCTGCCT	1192

Figure 20. (3 of 4)

gi 26327464 dbj AK031609.1	GTGCGCCTGGCAACGGCCATGATGGTGCCCTATACTCTGCCGCTGGAGAG	1094
gi 34861241 ref XM_341960.1	GTGCGCCTGGCCACTGCCATGATGGTACCCTATACTCTGCCACTGGAGAG	1109
gi 16878146 gb BC017280.1 BC01	GTGCGTCTGGCCACGGCCATGATGGTGCCCTACACGCTGCCGCTGGAGAG	1242

gi 26327464 dbj AK031609.1	TGCAGTGTCTTCACCATCCGCTTGTGGAGTGGCTGCCTGATGTCCCTG	1144
gi 34861241 ref XM_341960.1	CGCAGTGTCTTCACCATCCGTTTGTGGAGTGGCTGCCTGATGTCCCTG	1159
gi 16878146 gb BC017280.1 BC01	CGCTCTGTCTTCACCATCCGCTTGTGGAGTGGCTGCCGACGTTCCCG	1292
	**	
gi 26327464 dbj AK031609.1	AAGATATCCGGTGGATGAAAGAGCAGACGGGTAGCATCTGCCAGTATCTG	1194
gi 34861241 ref XM_341960.1	AGGATATCCGGTGGATGAAGGAGCAGACAGGTAGCATCTGCCAGTATCTG	1209
gi 16878146 gb BC017280.1 BC01	AGGACATCCGGTGGATGAAGGAGCAGACGGGCAGCATCTGCCAGTATCTG	1342
	* *	
gi 26327464 dbj AK031609.1	GTGATGAGGGCCAAAGAGGAAATTGGGTGACCATCTGCCTTCCAGACTGTC	1244
gi 34861241 ref XM_341960.1	GTGATGAGGGCCAAAGAGGAAATTGGGTGACCATCTACCTTCCAGACTGTC	1259
gi 16878146 gb BC017280.1 BC01	GTGATGCGCGCCAAAGAGGAAAGCTGGCAGGACCTGCCCTCCAGGCTGCC	1392

gi 26327464 dbj AK031609.1	TGAGCAGGTGGAAGTGCACGTGCCAGTCTCTGCCCTCTGTGCCACTGT	1294
gi 34861241 ref XM_341960.1	TGAGCAGGTGGAAGTGCACGTGCCAGTCTCTGCCCTCTGTGCCACTGT	1309
gi 16878146 gb BC017280.1 BC01	GGAGCAGGTGGAAGTGCACGTGCCAGTCTCTGCCCTCTGTGCCACTGT	1442

gi 26327464 dbj AK031609.1	CTTGCGCCACCTACAGTGAGGCCCTACCCAACTGGGTACGAAACAACCTC	1344
gi 34861241 ref XM_341960.1	CTTGCGCCACCTACAGTGAGGCCCTACCCAACTGGGTACGAAACAACCTC	1359
gi 16878146 gb BC017280.1 BC01	CCTGCGCCGCCCTACAGAGAGGCACTGCCCGCTGGATGCGCAACAACCTC	1492
	* *	
gi 26327464 dbj AK031609.1	TCACTGGGGGACGCGCTGGCCAAGTGGGAAGAATGCCAGCGTCAGTACT	1394
gi 34861241 ref XM_341960.1	TCACTGGGGGACGCGCTGGCCAAGTGGGAAGAATGCCAGCGTCAGTACT	1409
gi 16878146 gb BC017280.1 BC01	TCGCTGGGGGACGCGCTGGCCAAGTGGGAGAGTGGCAGCGCCAGTCTGCT	1542
	**	
gi 26327464 dbj AK031609.1	GCTGGGTCTCTTCTGCACCAATGTGGCCTTCCCGCGGATGCCCTTGC	1444
gi 34861241 ref XM_341960.1	GCTGGGTCTCTTCTGCACCAATGTGGCCTTCCCGCGTGTGCTTGC	1459
gi 16878146 gb BC017280.1 BC01	GCTCGGCTCTTCTGCACCAACGTGGCCTTCCCGCGGAGCTCTGC	1592

gi 26327464 dbj AK031609.1	TGCGCGCACCTGCCAGCCC-----CACTGCCGAGATCCTGCCACCCCA	1488
gi 34861241 ref XM_341960.1	TGCGCGCACCTGCCAGCCC-----CACCGCACAGATCCTGCCACCCCA	1503
gi 16878146 gb BC017280.1 BC01	TGCGCGCACCCCGCCGACCCGGCTCCCGCCCCGGGACCCAGCATCCCG	1642

gi 26327464 dbj AK031609.1	CAGGATCCAC----CTGGCCTCCCGCCTTGCTGAGAATCACCATTCCCAC	1534
gi 34861241 ref XM_341960.1	CAGGATCCAT----CTGGCCTCCCGCCTTGCTGA-----	1533
gi 16878146 gb BC017280.1 BC01	CAGCACCAGCTGGCGGGCCTGCCCTTGCTGAGCACCCTGCTCCCGA	1692

gi 26327464 dbj AK031609.1	ATCGCCCGGCTACCAGCCAAGCTCCAAGTTGTCTGCCCCACTAAGAGGA	1584
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	G--GCCCGGCGTGATCGGG-----GCCCTGGGGCTGTGAGA---	1728
gi 26327464 dbj AK031609.1	GCCCCGGGGTGGAAACAAGATCCTGTCTGCCCCGGCTCTCCCCCTTACATG	1634
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	-CCCCGACCTCTCGAGGAACC---CTGCCTGAGACGCTCCATTAC-CA	1773
gi 26327464 dbj AK031609.1	CTGTGGAATGAGGACATAGGACCTGCACAGCTGCAAGTGGGCTTTTCGAT	1684
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	CTGCGCAGTGAGATGAGGGGACTCACAGTTGCCAAGAG-GGGTCTTTGCC	1822

30/30

Figure 20. (4 of 4)

gi 26327464 dbj AK031609.1	GTGAAACCTTTCACCAGCCACTCACTATGCTACTCCTGGTGGGGAGGGAT	1734
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	GTGGGCCCCCTCGCCAGCCACTCACCA-GCTGCATGCACTGAGAGGGGAG	1871
gi 26327464 dbj AK031609.1	GGGAGTCGCCCTCCCCGGAGCCACAGAGCCCTCCCCCGTCACGTC--	1782
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	GTTTCCACACCCCTCCCCTGGGCGCTGAGGCCCGCGCACCTGTGCCTT	1921
gi 26327464 dbj AK031609.1	ACCTGTGCCTTACTCTGCCACCA--CCTTTTCAGTGCAGGGTCAGTCT	1830
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	AATCTTCCCTCCCCTGTGCTGCCCGAGCACCTCCCCCGCCCTTTACTCC	1971
gi 26327464 dbj AK031609.1	TAAGAACTCCACATCTGCTGCTGC-TCCCTGGTGTCCAAGTTTCCTTGCA	1879
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	TGAGAACTTTGCAGCTGCCCTTCCCTCCCGTTTTTCATGGCCTGCTGAA	2021
gi 26327464 dbj AK031609.1	GA--GTGTGTGAAGAATTATTTATTTTGCCTAAAGCAGATCTAATAAAAG	1927
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	ATATGTGTGTGAAGAATTATTTATTTTGCCTAAAGCAGATCTAATAAATG	2071
gi 26327464 dbj AK031609.1	CCACAGCTCAGCTTCTGCCTTCTCACTTCTGCATGCT-----	1965
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	CTGCAGCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2121
gi 26327464 dbj AK031609.1	- (SEQ ID NO:12)	
gi 34861241 ref XM_341960.1	- (SEQ ID NO:15)	
gi 16878146 gb BC017280.1 BC01	A 2122 (SEQ ID NO:1)	